



FIG. 1

ATGGCGGATTCCAGCGAAGGCCCCGCGCGGGGCCCCGGGGAGGTGGCTGAGCTCCCCGGGGATG
AGAGTGGCACCCAGGTGGGGAGGCTTTTCCTCTCTCCTCCCTGGCCAATCTGTTTGAGGGGGA
GGATGGCTCCCTTTGCCCCACCGGCTGATGCCAGTCGCCCTGCTGGCCAGGCGATGGGCGA
CCAAATCTGCGCATGAAGTTCCAGGGCGCCTTCCGCAAGGGGGTGCCCAACCCCATCGATCTGC
TGGAGTCCACCCTATATGAGTCCTCGGTGGTGCCTGGGCCCCAAGAAAGCACCCATGGACTCACT
GTTTGACTACGGCACCTATCGTCACCACTCCAGTGACAACAAGAGGTGGAGGAAGAAGATCATA
GAGAAGCAGCCGAGAGCCCCAAAGCTCCCGCCCCCTCAGCCGCCCCCATCCTCAAAGTCTTCA
ACCGGCCCATCCTCTTTGACATCGTGTCCCGGGGCTCCACTGCTGACCTGGACGGGCTGCTCCC
ATTCTTGCTGACCCACAAGAAACGCCTAACTGATGAGGAGTTTCGGGAACCATCTACGGGGAAG
ACCTGCCTGCCCAAGGCCCTTGCTGAACCTGAGCAATGGCCGCAACGACACCATCCCTGTGCTGC
TGGACATCGCGGAGCGCACCGGCAACATGAGGGAGTTCATTAACCTCGCCCTTCCGTGACATCTA
CTATCGAGGGCAGACAGCCCTGCACATCGCCATTGAGCGTCGCTGCAAACACTACGTGGAACCTT
CTCGTGGCCAGGGAGCTGATGTCCACGCCAGGCCCGTGGGCGCTTCTTCCAGCCCAAGGATG
AGGGGGGCTACTTCTACTTTGGGGAGCTGCCCTGTGCTGGCTGCCTGCACCAACCAGCCCCA
CATTGTCAACTACCTGACGGAGAACCCCCACAAGAAGGCGGACATGCGGCGCCAGGACTCGCGA
GGCAACACAGTGCTGCATGCGCTGGTGGCCATTGCTGACAACACCCGTGAGAACACCAAGTTTG
TTACCAAGATGTACGACCTGCTGCTGCTCAAGTGTGCCCGCCTCTTCCCCGACAGCAACCTGGA
GGCCGTGCTCAACAACGACGGCCTCTCGCCCCCTCATGATGGCTGCCAAGACGGGCAAGATTGGG
GTCTTTTACGACATCATCCGGCGGGAGGTGACGGATGAGGACACACGGCACCTGTCCCGCAAGT
TCAAGGACTGGGCCTATGGGCCAGTGATTTCTCGCTTTATGACCTCTCCTCCCTGGACACGTG
TGGGGAAGAGGCCTCCGTGCTGGAGATCCTGGTGTACAACAGCAAGATTGAGAACCGCCACGAG
ATGCTGGCTGTGGAGCCCATCAATGAACTGCTGCGGGACAAGTGGCGCAAGTTCGGGGCCGTCT
CCTTCTACATCAACGTGGTCTCCTACCTGTGTGCCATGGTCATCTTCACTCTCACCGCCTACTA
CCAGCCGCTGGAGGGCACACCGCCGTACCCTTACCGCACCCAGGTGGACTACCTGCGGCTGGCT
GGCGAGGTCAATTACGCTCTTCACTGGGGTCTGTTCTTCTTACCAACATCAAAGACTTGTTCA
TGAAGAAATGCCCTGGAGTGAATTCTCTCTTCAATTGATGGCTCCTTCCAGCTGCTCTACTTCAT
CTACTCTGTCTGTTGATCGTCTCAGCAGCCCTCTACCTGGCAGGGATCGAGGCCTACCTGGCC
GTGATGGTCTTTGCCCTGGTCTTGGGCTGGATGAATGCCCTTTACTTACCCGTGGGCTGAAGC
TGACGGGGACCTATAGCATCATGATCCAGAAGATTCTCTTCAAGGACCTTTTCCGATTCTGCT
CGTCTACTTGCTCTTTCATGATCGGCTACGCCTCAGCCCTGGTCTCCCTCCTGAACCCGTGTGCC
AACATGAAGGTGTGCAATGAGGACCAGACCAACTGCACAGTGCCCACTTACCCCTCGTGCCGTG
ACAGCGAGACCTTCAGCACCTTCCTCCTGGACCTGTTTAAAGCTGACCATCGGCATGGGCGACCT
GAGATGCTGAGCAGCACCAAGTACCCCGTGGTCTTCATCATCCTGCTGGTGACCTACATCATCC
TCACCTTTGTGCTGCTCCTCAACATGCTCATTGCCCTCATGGGCGAGACAGTGGGCCAGGTCTC
CAAGGAGAGCAAGCACATCTGGAAGCTGCAGTGGGCCACCACCATCCTGGACATTGAGCGCTCC
TTCCCCGTATTCTGAGGAAGGCCTTCCGCTCTGGGGAGATGGTCACCGTGGGCAAGAGCTCGG
ACGGCACTCCTGACCGCAGGTGGTGGTTCAGGGTGAATGAGGTGAACTGGTCTCACTGGAACCA
GAACTTGGGCATCATCAACGAGGACCCGGGCAAGAATGAGACCTACCAGTATTATGGCTTCTCG
CATAACCGTGGGCCGCTCCGCGAGGGATCGTGGTCTCGGTGGTACCCCGCGTGGTGGAACCTGA
ACAAGAACTCGAACCCGGACGAGGTGGTGGTGCCTCTGGACAGCATGGGGAACCCCCGCTGCGA
TGGCCACCAGCAGGGTTACCCCGCAAGTGGAGGACTGATGACGCCCGCTCTAGGGACTGCAG
CCCAGCCCCAGCTTCTCTGCCCACTCATTTCTAGTCCAGCCGATTTTACGAGTGCCCTTCTGGG
GTGTCCCCCACACCCTGCTTTGGCCCCAGAGGCGAGGGACAGTGGAGGTGCCAGGGAGGCCC
CAGGACCCTGTGGTCCCTGGCTCTGCCTCCCCACCCTGGGGTGGGGGCTCCCGGCCACCTGTC
TTGCTCCTATGGAGTCACATAAGCCA



FIG. 2

MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGED
GSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVNPIDLLESTLYESSVVPGPKKA
PMDSLFDYGTyrHHSSDNKRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSR
GSTADLDGLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAE
RTGNMREFINSFPRDIYYRGQTALHIAIERRCKHYVELLVAQGADVHAQARGRFFQPK
DEGGYFYFGELPLSLAACTNQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADN
TRENTKFVTKMYDLLLLKCARLEFPDSNLEAVLNNDGLSPLMMAAKTGKIGVFQHIIRR
EVTDEDTRHLSRKFKDWAYGPVYSSLYDLSSLDTCGEEASVLEILVYNSKIENRHEML
AVEPINELLRDKWRKFGAVSFYINVVSYLCAVIFTLTAYYQPLEGTPPYRTTVDY
LRLAGEVITLFTGVLFFFTNIKDLEFMKKCPGVNSLFIDGSFQLLYFIYSVLVIVSAAL
YLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLFRFLVYLLF
MIGYASALVSLNPCANMKVCNEDQTNCTVPTYPSCRDSETFSTFLDLFKLTIGMGD
LEMLSSTKYPVVFIIILLVTYIILTFVLLLNMLIALMGETVGQVSKEKHIWKLQWATT
ILDIERSFVFLRKAFRSGEMVTVGKSSDGTDDRWCFRVNEVNWSHWNQNLGIINED
PGKNETYQYYGFSHTVGRLRRDRWSSVVPVVELNKN SNPDEVVPLDSMGNPRCDGH
QQGYPRKWRTDDAPL

FIG. 3

AGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCC
AACGCGTTGGAGCTCTCCCATATGGTCGACCTGCAGCGGCCGCGAATTCAGTAGTGATTATGGC
GGATTCCAGCGAAGGCCCCCGCGCGGGGGCCCGGGGAGGTGGCTGAGCTCCCCGGGGATGAGAGT
GGCACCCAGGTGGGGAGGCTTTTCTCTCTCTCTCCCTGGCCAATCTGTTTGAGGGGGAGGATG
GCTCCCTTTTCGCCCTCACCGGCTGATGCCAGTCGCCCTGCTGGCCCAGGCGATGGGCGACCAA
TCTGCGCATGAAGTTCAGGGCGCCTTCGCGAAGGGGGTGCCCAACCCCATCGATCTGCTGGAG
TCCACCCTATATGAGTCCTCGGTGGTGCCTGGGCCCCAAGAAAGCACCCATGGACTCACTGTTTG
ACTACGGCACCTATCGTCAACCACTCCAGTGACAACAAGAGGTGGAGGAAGAAGATCATAGAGAA
GCAGCCGAGAGCCCCAAAGCCCCCTGCCCTCAGCCGCCCCCATCCTCAAAGTCTTCAACCGG
CCTATCCTCTTTGACATCGTGTCCCGGGGCTCCACTGCTGACCTGGACGGGCTGCTCCCATTTCT
TGCTGACCCACAAGAAACGCCTAACTGATGAGGAGTTTCGAGAGCCATCTACGGGGAAGACCTG
CCTGCCCAAGGCCTTGCTGAACCTGAGCAATGGCCGCAACGACACCATCCCTGTGCTGCTGGAC
ATCGCGGAGCGCACCGGCAACATGCGGGAGTTCATTAACCTCGCCCTTCCGTGACATCTACTATC
GAGGTCAGACAGCCCTGCACATCGTCATTGAGCGTCGCTGCAAACACTACGTGGAACCTTCTCGT
GGCCCAGGGAGCTGATGTCCAGCCCCAGGCCCGTGGGCGCTTCTTCCAGCCCAAGGATGAGGGG
GGCTACTTCTACTTTGGGGAGCTGCCCCGTGTCGCTGGCTGCCTGCACCAACCAGCCCCACATTG
TCAACTACCTGACGGAGAACCCCCACAAGAAGGCGGACATGCGGCGCCAGGACTCGCGAGGCAA
CACAGTGCTGCATGCGCTGGTGGCCATTGCTGACAACACCCGTGAGAACACCAAGTTTGTACC
AAGATGTACGACCTGCTGCTGCTCAAGTGTGCCCGCCTCTTCCCCGACAGCAACCTGGAGGCCG
TGCTCAACAACGACGGCCTCTCGCCCCCTCATGATGGCTGCCAAGACGGGCAAGATTGGGATCTT
TCAGCACATCATCCGGCGGGAGGTGACGGATGAGGACACACGGCACCTGTCCCGCAAGTTCAAG
GACTGGGCCTATGGGCCAGTGATTCTCGCTTTATGACCTCTCCTCCCTGGACACGTGTGGGG
AAGAGGCCTCCGTGCTGGAGATCCTGGTGTACAACAGCAAGATTGAGAACCGCCACGAGATGCT
GGCTGTGGAGCCCATCAATGAACTGCTGCGGGACAAGTGGCGCAAGTTCGGGGCCGTCTCCTTC
TACATCAACGTGGTCTCCTACCTGTGTGCCATGGTCATCTTCACTCTCACCGCCTACTACCAGC
CGCTGGAGGGCACACCGCCGTACCCCTACCGCACACGGTGGACTACCTGCGGCTGGCTGGCGA
GGTCATTACGCTCTTCACTGGGGTCTGTTCTTCTTCAACCAACATCAAAGACTTGTTCATGAAG
AAATGCCCTGGAGTGAATTCTCTCTTCAATTGATGGCTCCTTCCAGCTGCTCTACTTCACTACT
CTGTCTTGGTGATCGTCTCAGCAGCCCTCTACCTGGCAGGGATCGAGGCCCTACCTGGCCGTGAT
GGTCTTTGCCCTGGTCTTGGGCTGGATGAATGCCCTTTACTTCAACCGTGGGCTGAAGCTGACG
GGGACCTATAGCATCATGATCCAGAAGATTCTCTTCAAGGACCTTTTCCGATTCTGCTCGTCT
ACTTGCTCTTCAATGATCGGCTACGCTTACGCCCTGGTCTCCCTCCTGAACCCGTGTGCCAACAT
GAAGGTGTGCAATGAGGACCAGACCAACTGCACAGTGCCCACTTACCCCTCGTGCCGTGACAGC
GAGACCTTACGACCTTCTCCTGGACCTGTTTAAGCTGACCATTGGCATGGGCGACCTGGAGA
TGCTGAGCAGCACCAAGTACCCCGTGGTCTTCATCATCCTGCTGGTGACCTACATCATCCTCAC
CTTTGTGCTGCTCCTCAACATGCTCATTGCCCTCATGGGCGAGACAGTGGGCCAGGTCTCCAAG
GAGAGCAAGCACATCTGGAAGCTGCAGTGGGCCACCACCATCCTGGACATTGAGCGCTCCTTCC
CCGTATTCTTGAGGAAGGCCTTCCGCTCTGGGGAGATGGTCAACCGTGGGCAAGAGCTCGGACGG
CACTCCTGACCGCAGGTGGTGCTTCAGGGTGGATGAGGTGAACTGGTCTCACTGGAACCAGAAC
TTGGGCATCATCAACGAGGACCCGGGCAAGAATGAGACCTACCAGTATTATGGCTTCTCGCATA
CCGTGGGCCCGCCTCCGCAGGGATCGCTGGTCTCGGTGGTACCCCGCGTGGTGGAACTGAACAA
GAACTCGAACCCGGACGAGGTGGTGGTGCCTCTGGACAGCATGGGGAACCCCGCTGCGATGGC
CACCAGCAGGGTTACCCCGCAAGTGGAGGACTGATGACGCCCCGCTCTAGGGACTGCAGCCCA
GCCCCAGCTTCTCTGCCCCTCACTTCTAGTCCAGCCGCATTTACGAGTGCCCTTCTGGGGTGT
CCCCCACACCCTGCTTTGGCCCCAGAGGCGAGGGACCAGTGGAGGTGCCAGGGAGGGCCCCAGG
ACCCTGTGGTCCCCTGGCTCTGCCTCCCCACCCTGGGGTGGGGGCTCCCGGCCACCTGTCTTGC
TCCTATGGAATCACTAGTGAATTCCCGCGGCCGCCATGGCGGCCGGGAGCATGCGACGTGGGGC
CCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTGTTTTACAACGTGCTGACTG
GGAAACCTGCGTTACCCAACCTTAATCGCCTTGACGACATCC



FIG. 4

MADSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANL
FEGEDGSLSPSPADASRPAGPGDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPGPKKAP
MDSLEFDYGTYRHSSDNKRWRKKIIEKQPQSPKAPAPQPPILKVFNRPILFDIVSRGSTADLD
GLLPFLLTHKKRLTDEEFREPSTGKTCLPKALLNLSNGRNDTIPVLLDIAERTGNMREFINSF
RDIYYRGQTALHIVIERRCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAACT
NQPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLFPD
SNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYDLSS
LDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTL
TAYYQPLEGTPPYPPYRTTVDYLRRLAGEVITLFTGVLFFFTNIKDLFMKKCPGVNSLFIDGSFQL
LYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTGTYSIMIQKILFKDLF
RFLLVYLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTYPSCRDSETFSTFLDLFKLTIG
MGDLEMLSSTKYPVVFIIILLVTYIILTFVLLNMLIALMGETVGQVSKEKHIWKLQWATTILD
IERSEFPVFLRKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNWSHWNQNLGIINEDPGKNETYQY
YGFSTVGRRLRRDRWSSVPRVVELNKNNSNPDEVVPLDSMGNPRCDGHQQGYPRKWRTDDAPL

FIG. 5A

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

Secondary structure

[illegible]

	60	70	80	90	100
PVD	ASRRP	NLRMKF	QGAFRKGV	DLLEST	YESSVVPPK
RWT	ASRRP	NLRMKf	SFAFRKGV	DLLEST	YESSVVPPK
PAD	ASRRP	NLRMKF	QGAFRKGV	DLLEST	YESSVVPPK
PSR	GAG-	DGKK	HGAFRKGP	MELLEST	YESSVVAPK

	110	120	130	140	150
KAPMDSL	FDYGTYRH	HPSDNKRWR	RKVVEKQSP	KAPQPPP	LKVFN
KAPMDSL	FDYGTYRH	HPSDNKRWR	RKVVEKQSP	KAPQPPP	LKVFN
KAPMDSL	FDYGTYRH	HPSDNKRWR	KKLEKQSP	KAPQPPP	LKVFN
KAPMDSL	FDYGTYRH	HPSDNKRWR	RRVVEKPVAGT	KGPAPNPPPV	LKVFN
				AGEKPPRL	YD
					DRE

52

1

FIG. 5B

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

Secondary structure

160 170 180 190 200
RPI LFDI VSRGSTADL DGLLSY LLTHKKRLTDEEFREPSTGKTCLPKALL
RPI LFDI VSRGSTADL DGLLSY LLTHKKRLTDEEFREPSTGKTCLPKALL
RPI LFDI VSRGSTADL DGLLSY LLTHKKRLTDEEFREPSTGKTCLPKALL
RPI LFDI VSRGSTADL DGLLSY LLTHKKRLTDEEFREPSTGKTCLPKALL
RRSTFDVAQSNCGELLESLLPFLQRWSKYLLTDSAYTEGSTGKTCLPKALL
RDRLFSVMVRGVPEELTGLLE PLGKWEDEHKACWQMQRGALGESLHVLN
R I FshVupussittLpuLLsaLhccKcLT DptaccsutGKTCL KAIL

210 220 230 240 250
NLSNGRNDTI PVLLDI AERTGNMREFINSPPFRDI YYRGQTALHI AERRC
NLSNGRNDTI PVLLDI AERTGNMREFINSPPFRDI YYRGQTALHI AERRC
NLSNGRNDTI PVLLDI AERTGNMREFINSPPFRDI YYRGQTALHI AERRC
NLSAGRNDTI PILLDI AEKTGNMREFINSPPFRDI YYRGQTALHI AERRC
NLSHNGQNDTI ALLLDVARKTDSLPKQFVNASTDESEYYKGGTALHI AERRC
NLQDGVNACI MP LQIDKDSGNPKPLVNACQCTDESEYYKGGTALHI AERRC
REQQVCYE ARVLLKR----- FPGMANDIYLGDEEQFGQSALHLAI VHDD
CDSKVHTKLARVLLRV----- FPNLALDVMIEGE EYLGASALHLSLAYSN
NLpsGpNcsi ILLclscoss hcp hNusapD aYpGQoALHI AERRC
AR

260 270 280 290 300
KHYVELLVAQGADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHI
KHYVELLVAQGADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHI
KHYVELLVAQGADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHI
KHYVELLVEIKGADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHI
MTLLVLLVNGADVQAANCGDFFKKTGGRPGFFYFGEPLSLAACTNQPHI
LQCVKLLVNGADVHLRAACGRFFQKH-QGTCTFYFGEPLSLAACTNQPHI
YETVSLLENSKADVNAACGNFFLPEDEKLTnvyYGEYPLAAACFQGNKDI
NELVADLIEAGADIHQRAIGSFFLPRDQQRANvMGEYPLAAACFQGNKDI
hchVpLLVipGADVHApGcFFpPcDptshFYFGEPLSLAACTsQci
D1 ADR2

FIG. 5C

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

```

310 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLL
320 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLL
330 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLL
340 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLL
350 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLL
VsaLhcNsapADhctQDSHGNTVLHALVhiADNo cNot aVopMYshL

```

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

```

360 LKCSRRLFPDSSNLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTTDEDTIR
370 LKCSRRLFPDSSNLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTTDEDTIR
380 LKCSRRLFPDSSNLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTTDEDTIR
390 LKCSRRLFPDSSNLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTTDEDTIR
400 LKCSRRLFPDSSNLETVLNNDGLSPLMMAAKTGKIGVFQHIIRREVTTDEDTIR
hcsucLhPssPLEtINpsGLOPLhAAKpGKtIFpalcRehtthc

```

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

```

410 HLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML
420 HLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML
430 HLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML
440 HLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML
450 HLSRKFKDWAYGPVYSSLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML
PLSRKFTTEWCYGPVRLNLTLPDGTINWNSALFELNGTKPEHLDML
REFWRYSNITCSGYPLNALDLPDGTINWNSALFELNGTKPEHLDML
cLSRKFPcWsYGPVhssLYDLSSLDTCGEEVSVLEILVYNSKIENRHEML

```

Secondary structure

TRADE MARK

460	470	480	490	500																																					
AV	EP	NE	LL	RD	KW	RK	F	G	A	V	S	F	Y	I	N	V	S	Y	L	C	A	M	V	I	F	T	L	T	A	Y	Y	Q	P	L	E	G	T	P	P	Y	
AV	EP	NE	LL	RD	KW	RK	F	G	A	V	S	F	Y	I	N	V	S	Y	L	C	A	M	V	I	F	T	L	T	A	Y	Y	Q	P	L	E	G	T	P	P	Y	
AV	EP	NE	LL	RD	KW	RK	F	G	A	V	S	F	Y	I	N	V	S	Y	L	C	A	M	V	I	F	T	L	T	A	Y	Y	Q	P	L	E	G	T	P	P	Y	
AV	EP	NE	LL	RD	KW	RK	F	G	A	V	S	F	Y	I	N	V	S	Y	L	C	A	M	V	I	F	T	L	T	A	Y	Y	R	P	M	E	G	P	P	P	Y	
LV	EP	LN	RL	LD	KW	DR	F	V	K	R	I	F	F	N	F	F	V	Y	C	L	Y	M	I	F	T	A	A	A	Y	Y	R	P	V	E	G	L	P	P	Y		
VL	EP	LN	KL	LE	KW	DR	F	V	S	R	I	F	F	N	F	A	C	L	V	Y	M	E	I	F	T	V	V	A	Y	H	Q	P	S	L	D	Q	P	P	S		
GS	EV	I	QR	LL	AD	KW	KA	F	A	Q	R	K	L	E	R	L	V	L	I	V	Q	L	L	I	L	S	I	V	V	Y	R	P	T	E	L	P	R	L	Y		
DG	GI	I	QR	LL	EE	KW	K	T	F	A	Q	N	Q	F	L	K	R	L	L	L	S	T	H	L	L	C	L	S	V	S	V	Y	R	P	A	H	D	G	E	A	E
S	EP	N	C	L	P	D	K	W	c	F	u	t	h	p	F	a	h	s	i	s	y	s	t	M	I	F	T	I	s	A	Y	a	p	P	h	E	s	s	P	P	Y

510	520	530	540	550																									
PYRTTV	VDYLR	LAGEV	ITL	TGV	LFFF	TSI	KDLF	MKKCP	GVNS	LF	VDGS	FFQ																	
PYRTTV	VDYLR	LAGEV	ITL	FTGV	LFFF	TSI	KDLF	MKKCP	GVNS	LF	VDGS	FFQ																	
PYRTTV	VDYLR	LAGEV	ITL	FTGV	LFFF	TNI	KDLF	MKKCP	GVNS	LF	VDGS	FFQ																	
PYRTTV	VDYLR	LAGEV	ITL	FTGV	LFFF	SNI	KDLF	MKKCP	GVNS	LF	VDGS	FFQ																	
KLKNTV	VGDDY	ITV	TGEI	LSV	SGGV	YFFF	-RG	QYF	LQRRP	SL	KSL	FVDS	YSSE																
SKATF	GESML	L	L	GGI	YL	L	GGI	W	YF	WRRRI	FI	W	SFMD	SYEE															
MEDPQ	WD	DY	Ia	CELL	LT	L	NCI	FFV	GYQQ	GEI	RT	QGM	RGY	L	RNL	KT	APAK												
DEDSE	GS	DA	SA	AA	LI	t	LV	GV	LSY	VI	EQQG	GEI	KN	QGL	SA	FL	KOL	SHAPAK											
shc	opsc	hpl	s	Gcl	l	h	ls	G	h	h	F	o	l	c	F	h	p	c	s	u	i	p	F	h	D	u	s	h	p

[illegible]

Secondary structure

FIG. 5E

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

610 620 630 640 650
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVTLLNPGCTNMMKV GNEEDQS
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVTLLNPGCTNMMKV GNEEDQS
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVTLLNPGCTNMMKV GNEEDQS
TYSI MI QKI LFKDLFRFLLVYLLFMI GYASALVTLLNPGCTNMMKV GNEEDQS
IYAVMI EKV LRDLCRFMFVYLVFLFGFSAVVTLEEDGKNNSLPMESTP
IYAVMI EKV LRDLCRFMFVYLVFLFGFSAVVTLEEDGKNNSLPMESTP
PFVQMI YSMI AGDMIRFAIISAIFLVSFQVFFYVVGKDMAKQKLEDTNP
PFVQMI YSMI AGDMIRFAIISAIFLVSFQVFFYVVGKDMAKQKLEDTNP
sYul MI pKhlhcDLhRfhlVYLI FhGausAlVolhpsst s phspcsp s

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

660 670 680 690 700
NCTVPSYPACRDSSEETFSAFLLDLF KLTIGMGDLMLSSAKYPVVFILLLV
NCTVPSYPACRDSSEETFSAFLLDLF KLTIGMGDLMLSSAKYPVVFILLLV
NCTVPSYPACRDSSEETFSAFLLDLF KLTIGMGDLMLSSAKYPVVFILLLV
NCTVPSYPACRDSSEETFSAFLLDLF KLTIGMGDLMLSSAKYPVVFILLLV
HKCRGSACKgNSYNSLYSTCLLELF KFTIGMGDLMLSSAKYPVVFILLLV
TIVTEQPTVIGQepYRSLLDASLELF KFTIGMGDLMLSSAKYPVVFILLLV
HACRI SGYTIYTYNTFPETFI TLFRA SMGGYDYEEFSCANYQALTKTLFV
... H PQVQSTMENTYTSTWMALEFQTTLGDYNYPD LNQTYPNLSKTVEF
pssh ohssps pIasshhlcLFKhTIGMGDL Ehhpscy sVhILLLV

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

710 720 730 740 750
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
TYIILTFVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
AYVLLTYVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
AYVLLTYVLLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
LYMFVMPIMMLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
LYMFVMPIMMLNMLIALMGETVGGVSKESKHIWKLQWATTI LDIERSFPPV
sYIILTLT a LLLNMLIALMGETVspVucpScclWKLQaApoilcLERSa h

Secondary structure

FIG. 5F

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

760 770 780 790 800
FLRKAFRSGEMVT VGKSS DGTPDRRWCGRVDEVNWSHWNQNLGI NEDPPG
FLRKAFRSGEMVT VGKSS DGTPDRRWCGRVDEVNWSHWNQNLGI NEDPPG
FLRKAFRSGEMVT VGKSS DGTPDRRWCGRVDEVNWSHWNQNLGI NEDPPG
FLRKAFRSGEMVT VGKSS DGTPDRRWCGRVDEVNWSHWNQNLGI NEDPPG
CRRKKHREGRLKVGTRGDTDEGRWCGRVDEVNWSHWNQNLGI NEDPPG
CRRKKHREGRLKVGTRGDTDEGRWCGRVDEVNWSHWNQNLGI NEDPPG
ADAKGYLEAYSIP LGPSDDSGFEVRGVMT KSKSKTRAKCRKGAVS NWKR
hRku aRp Gchl pVGpss DGss DhRWCGRVc EVNWop Wp Qs GhI s EDPG

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

810 820 830 840 850
KSEIYQYYGFSSHT MGRLLRRDRWSS VVPRVVELNKNSSGT DEVVVPPLDNLGN
KSEIYQYYGFSSHT MGRLLRRDRWSS VVPRVVELNKNSSAD DEVVVPPLDNLGN
KNEIYQYYGFSSHT MGRLLRRDRWSS VVPRVVELNKNSSNP DEVVVPPLDNLGN
KSDTIYQYYGFSSHT MGRLLRRDRWSS VVPRVVELNKNSSCPTE DEVVVPPLDNLGN
NcGVKRTLSFSLRSGRVSGRNWKn pLLRDASTDRHATQQEEVQLKHY
GPGITGNKKNPTSKPGK
LMVILKQTKTRARQRKQAI YNWKT GRKVI HTI D K VGT E QA VLL L H - GH
VGRVTLTALKKRGMTGE - EMRRL MWGRA SI SSPV KVT KCKL KDPY NL HT
t st l h p h h t h s p s h s c h t h c p W p s h h R s s p h c p p s s c p h l l t p h t p

Secondary structure

RnVR-MAC
MmVR-MAC
HsVR-MAC
GgVR-MAC
RnVR1
RnVRL-1
CeOSM-9
DmCG4536
Consensus
Regions

860 870
PNC DGHQHQGYAPK WRAEDAPL
PNC DGHQHQGYAPK WRTDDAPL
PNC DGHQHQGYAPK WRTDDAPL
AEARIE RHGQTIPS - - - - S
DRLDRVYEDH
S

97.2 %
94.8 %
82.5 %
39.8 %
35.2 %
17.0 %
15.4 %

Secondary structure

AGENT & TRADEMARK OFF

FIG. 6A

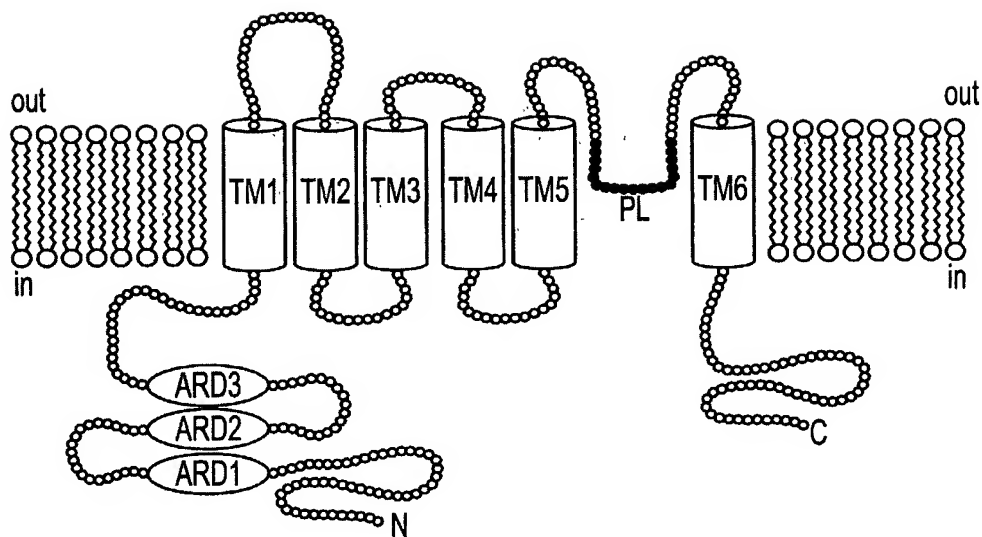


FIG. 6B

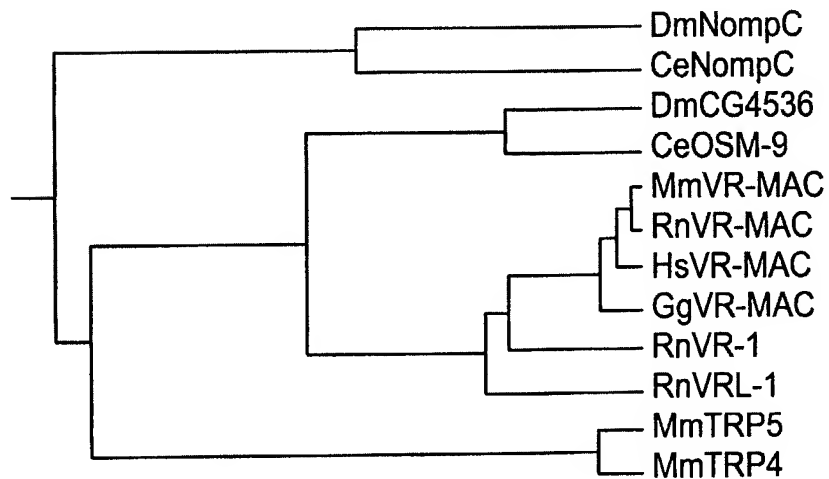




FIG. 7A

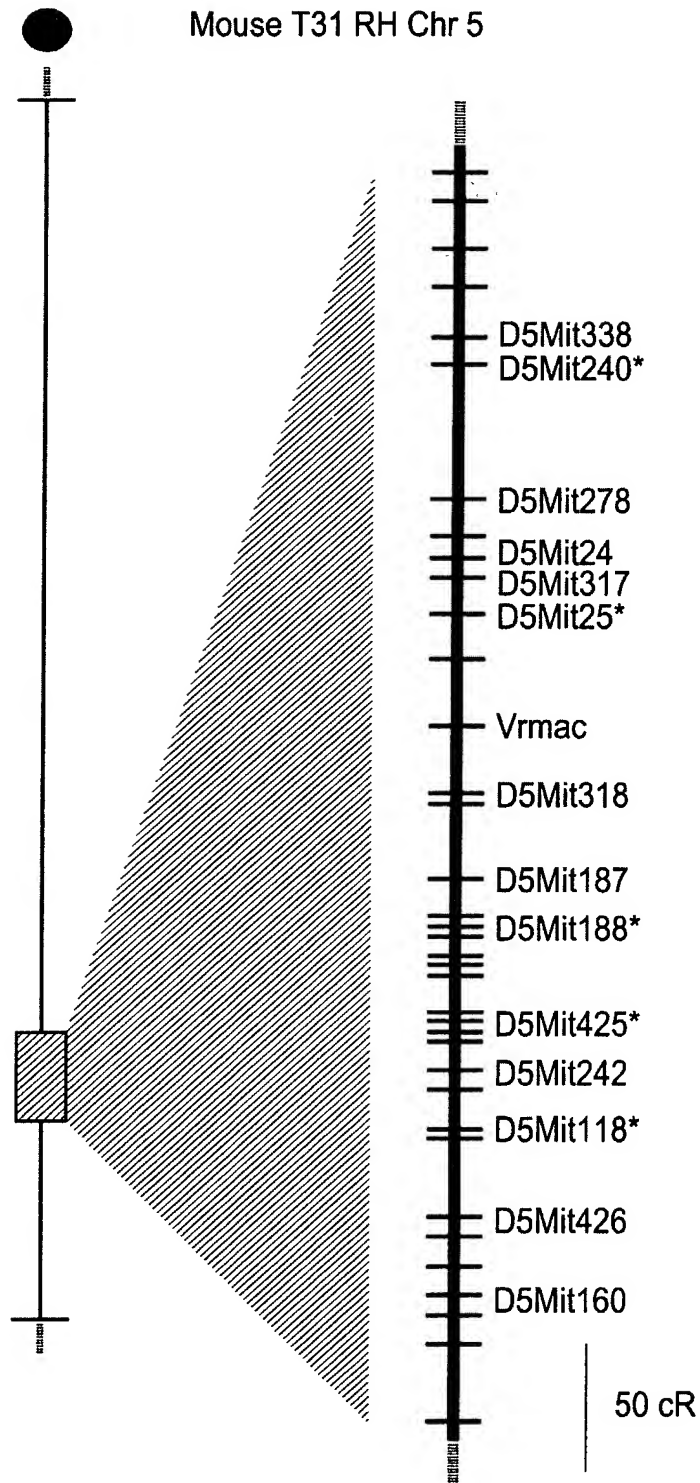




FIG. 7B

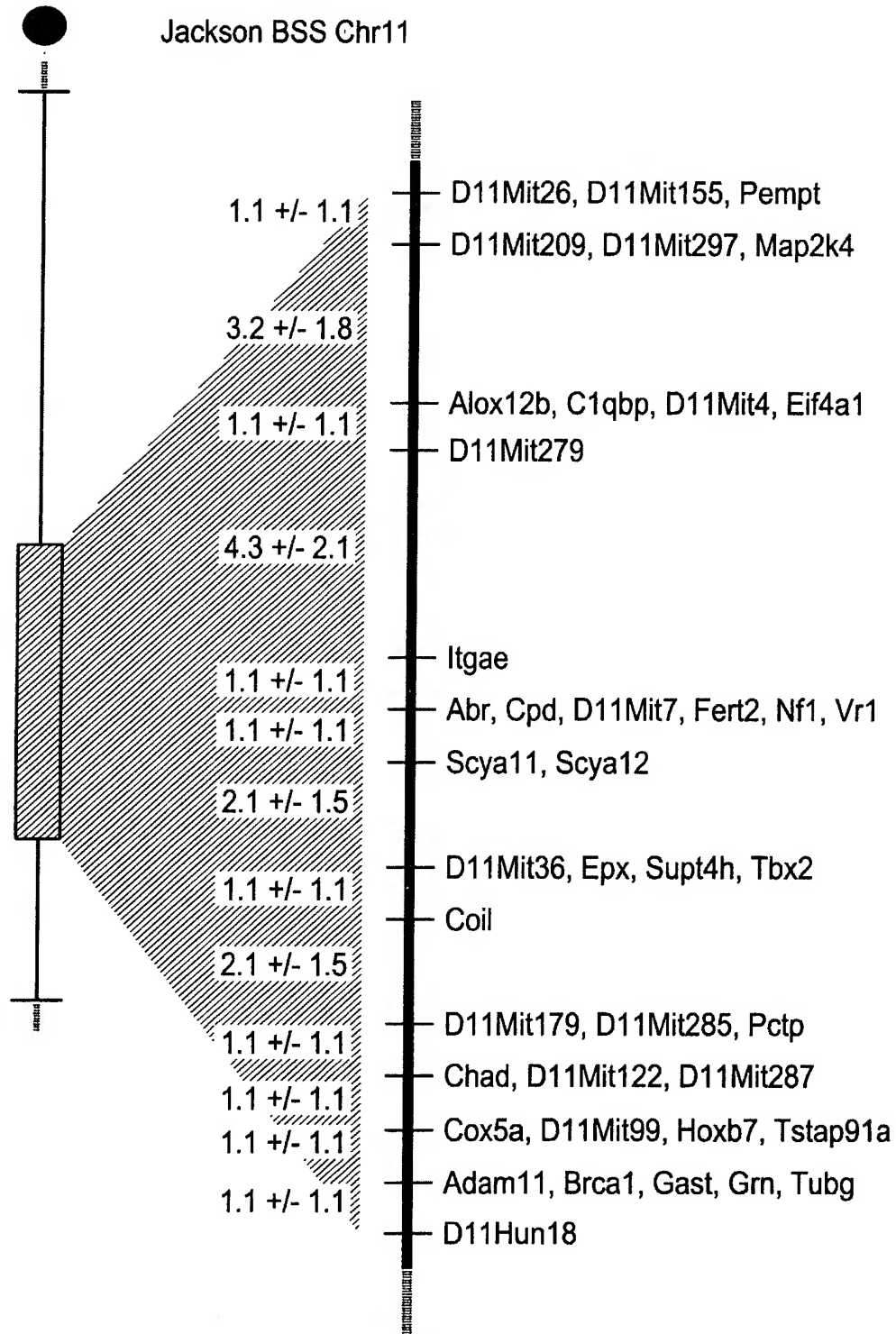
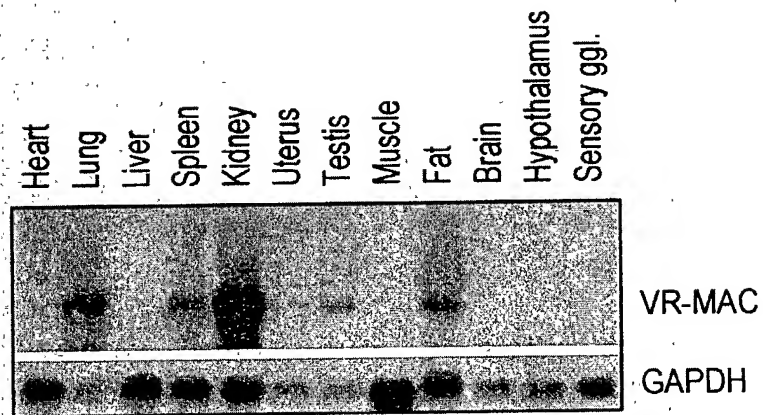


FIG. 8



PATENT & TRADE-MARK

FIG. 9A

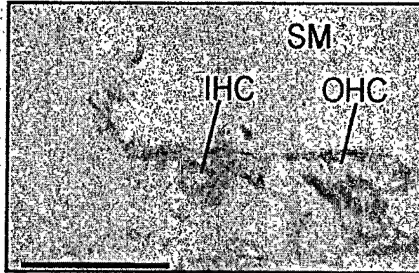


FIG. 9B

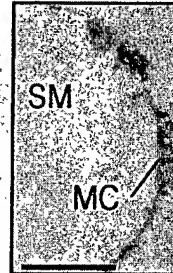


FIG. 9E

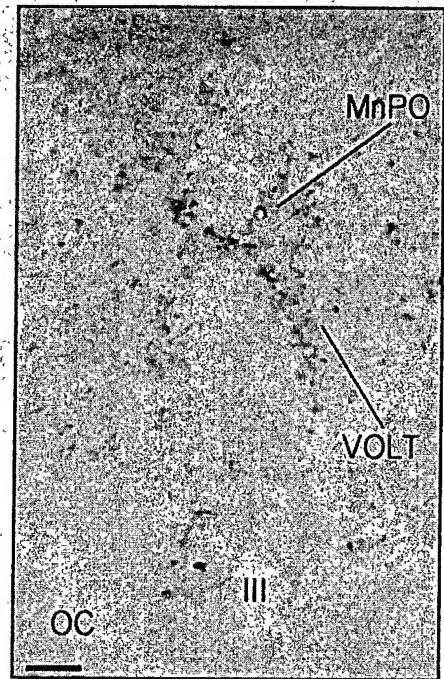


FIG. 9C



FIG. 9D

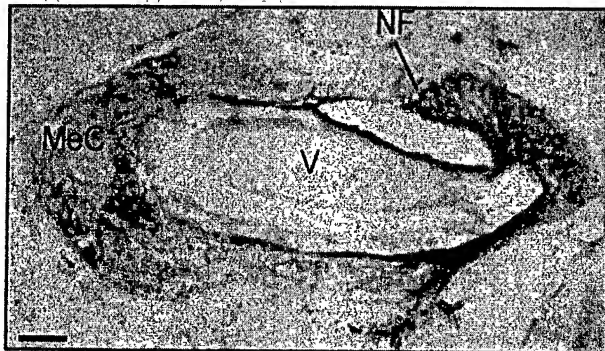


FIG. 9F

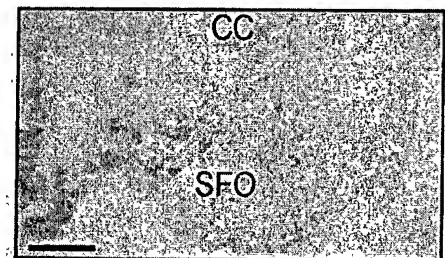


FIG. 9G

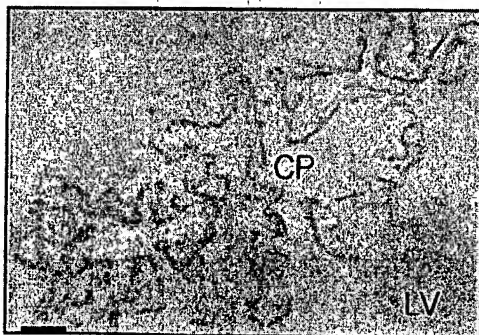
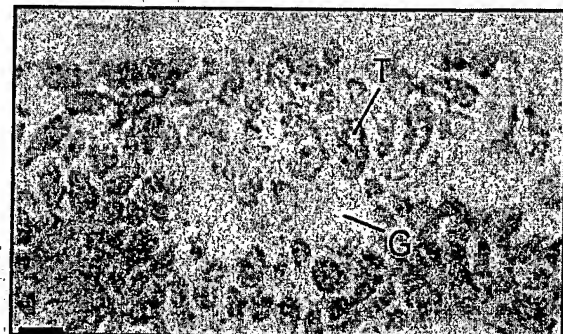


FIG. 9H



PATENT & TRADE-MARK OFFICE

FIG. 10A

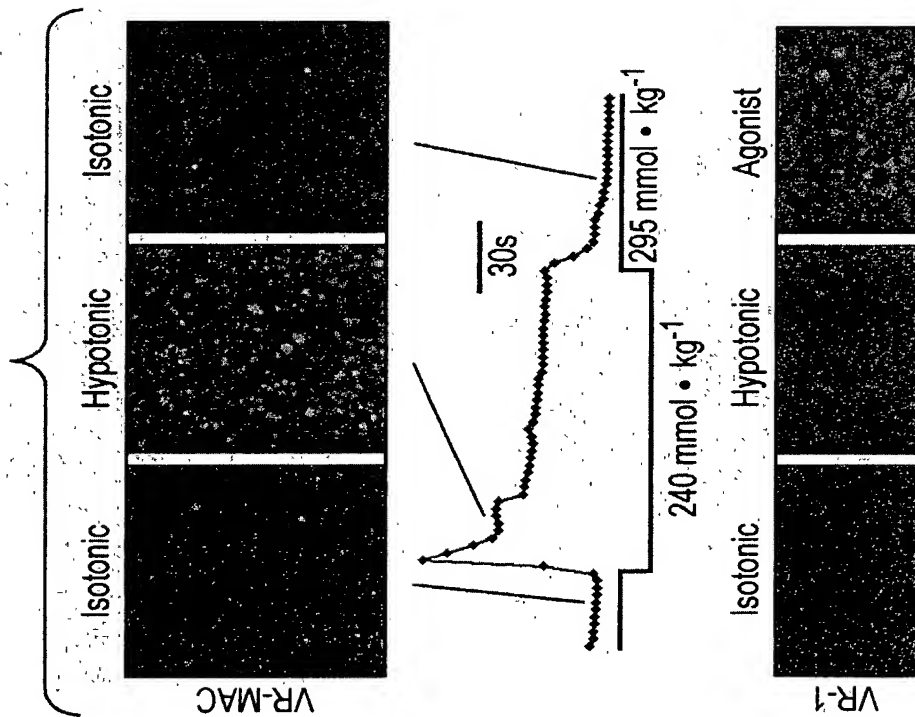


FIG. 10B

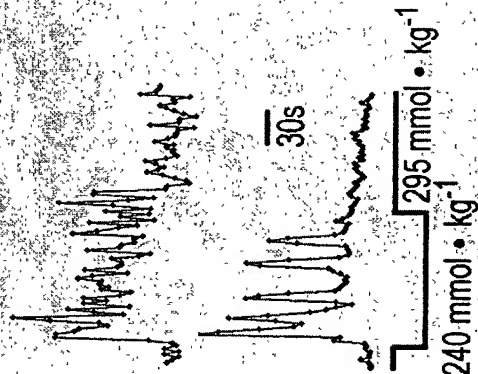
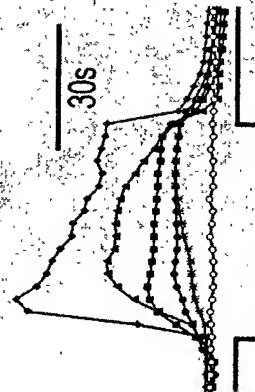


FIG. 10C



PATENT & TRADE-MARK OFF

FIG. 10D

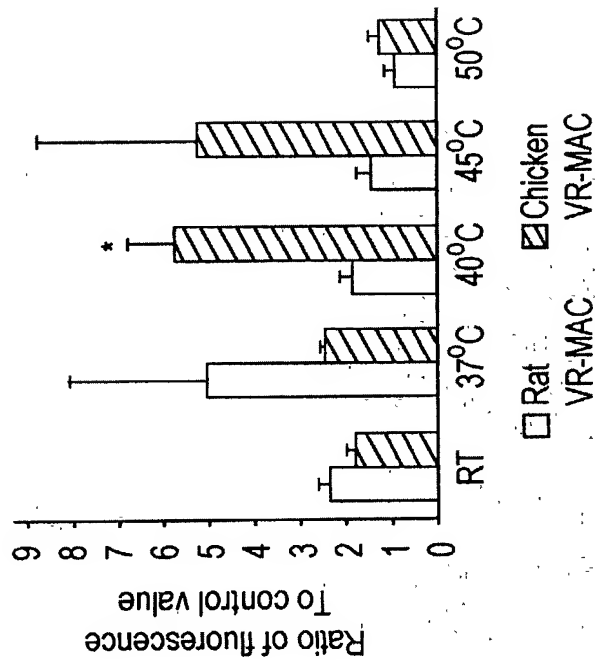


FIG. 10E

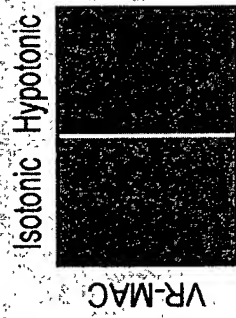


FIG. 10F

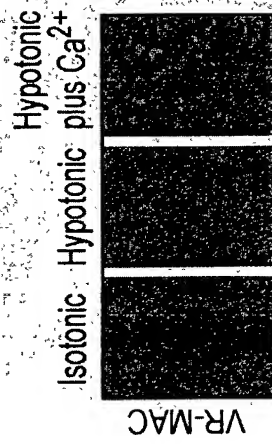




FIG. 11A

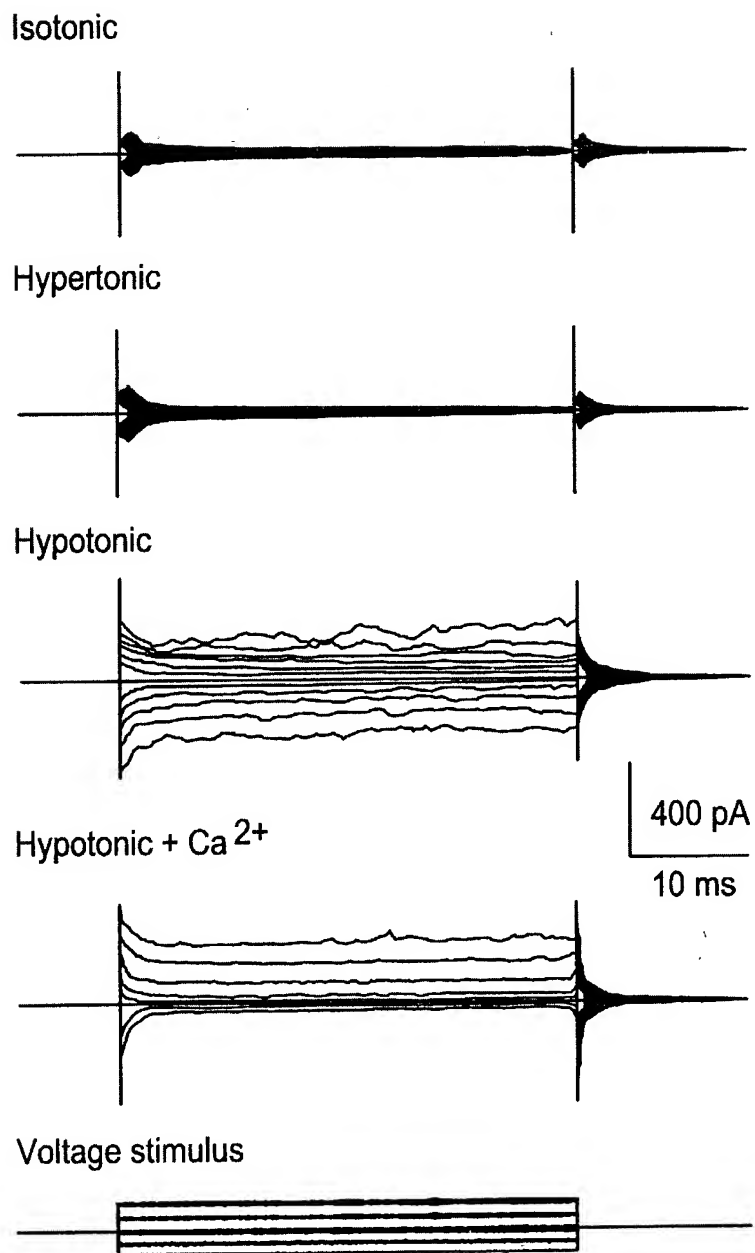




FIG. 11B

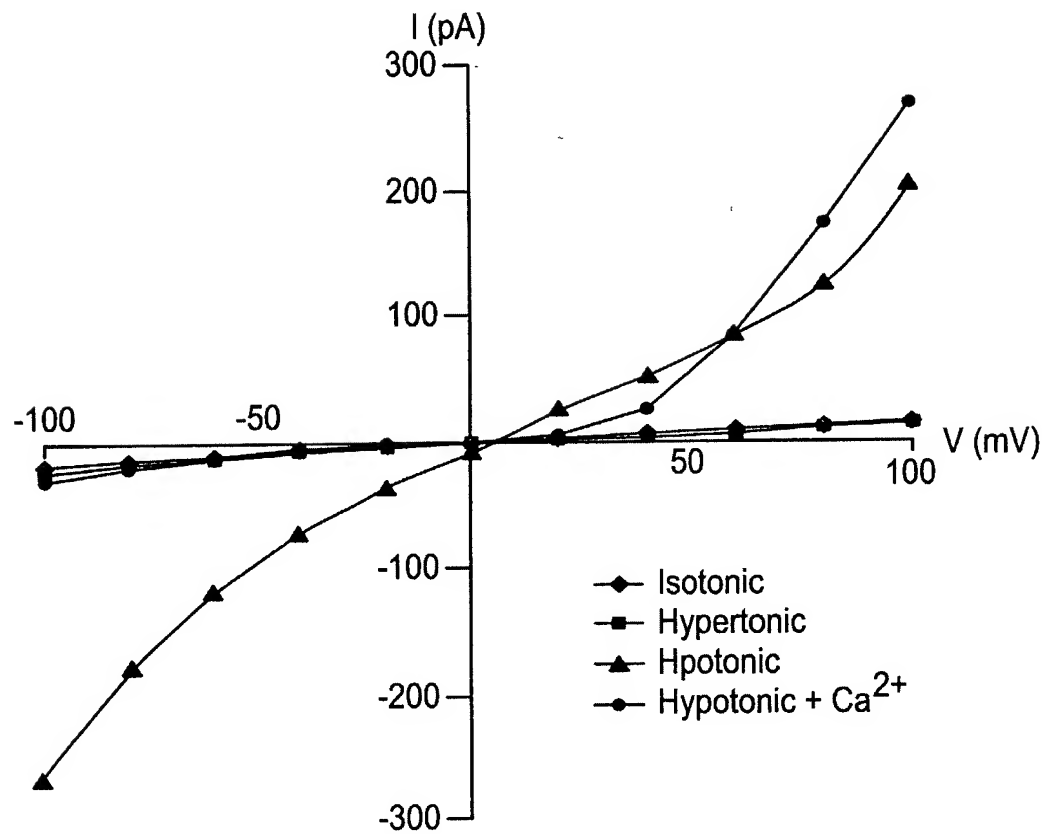
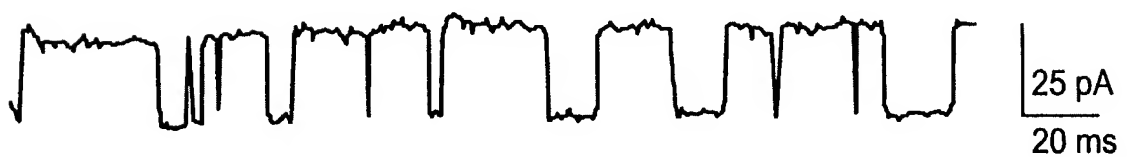
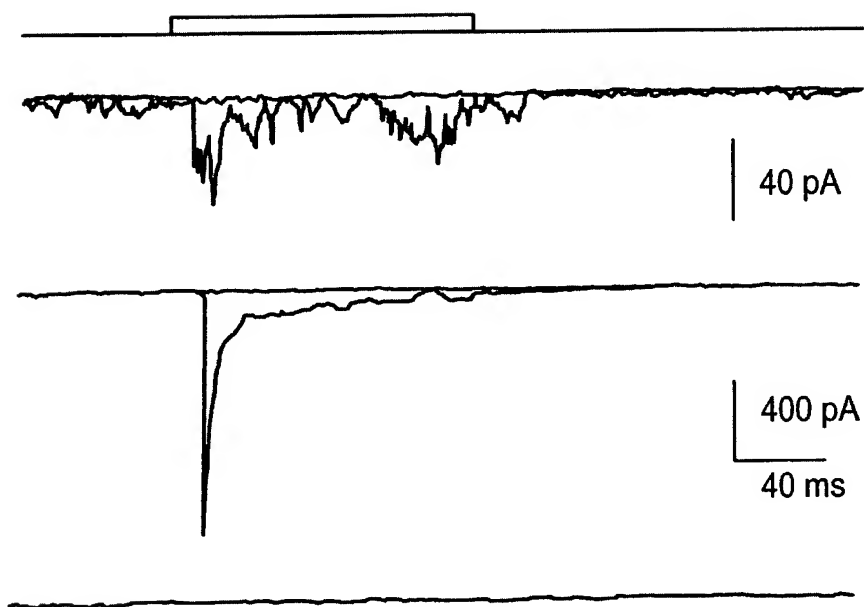


FIG. 11C



PATENT & TRADE MARK OFF

FIG. 12



PT & TRADEMARK OFFICE

FIG. 13A

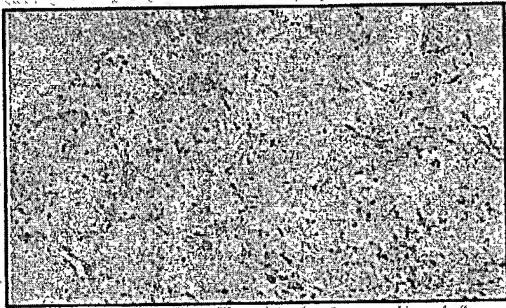


FIG. 13B

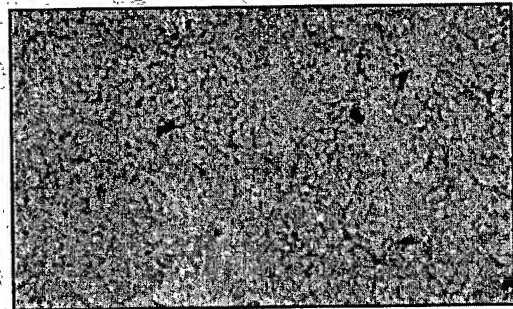


FIG. 13C

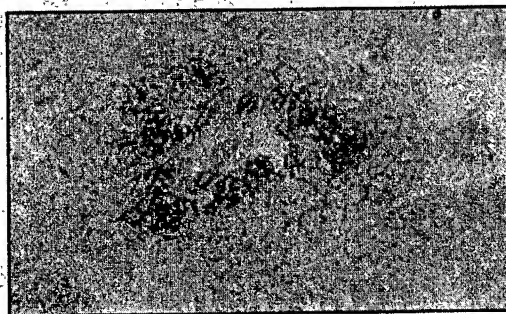


FIG. 13D

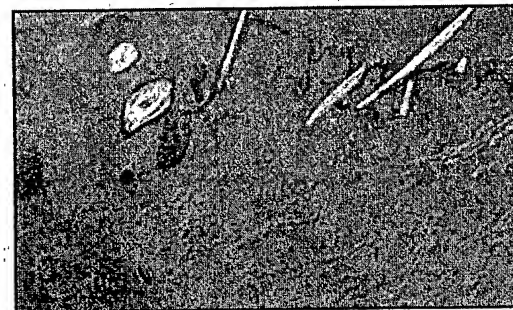


FIG. 13E

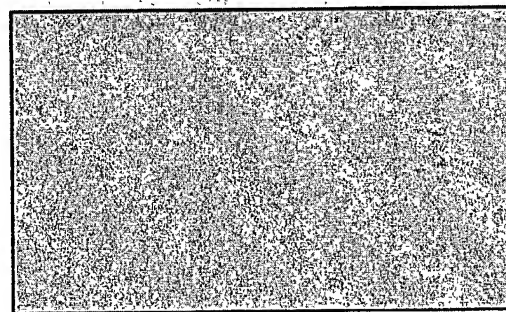
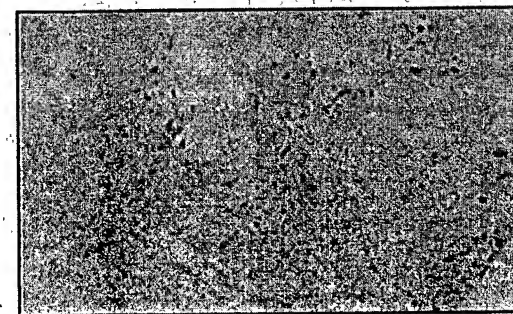


FIG. 13F



PATENT & TRADE-MARK OFF

FIG. 13G

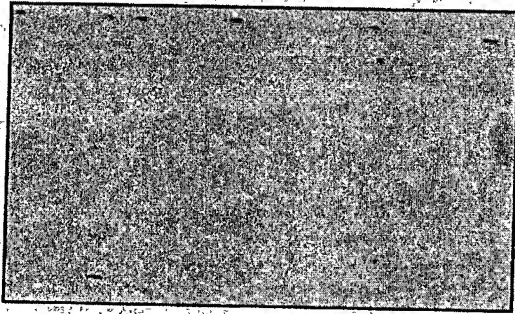


FIG. 13H

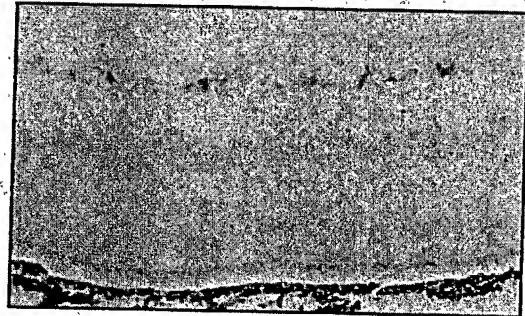


FIG. 13I

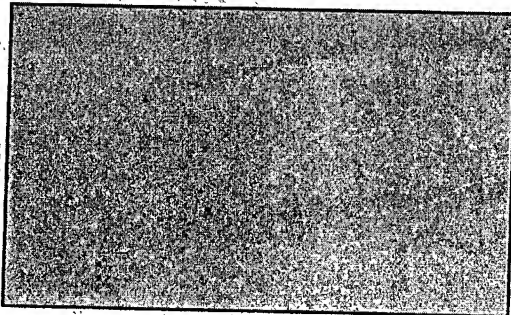
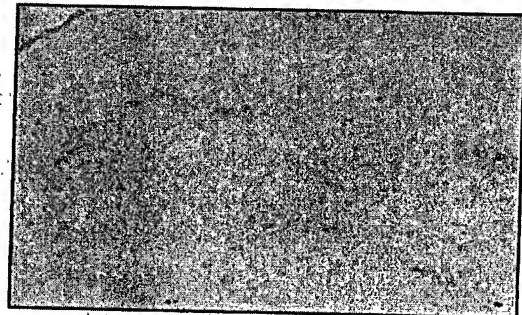


FIG. 13J



PATENT & TRADEMARK OFFICE

FIG. 14A-1

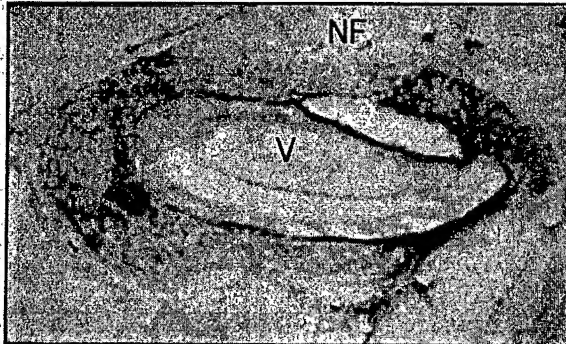


FIG. 14A-2

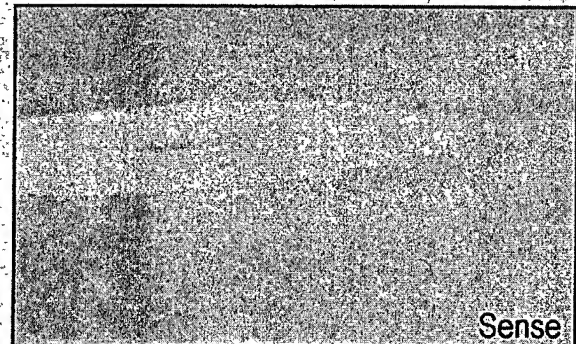


FIG. 14B-1

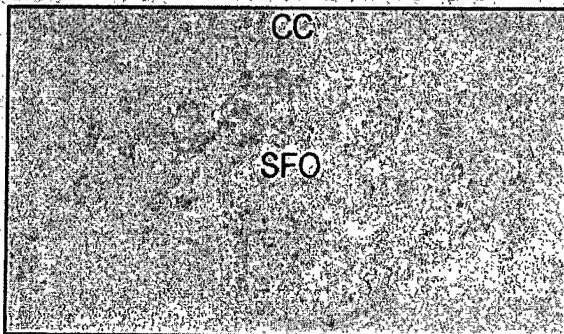


FIG. 14B-2

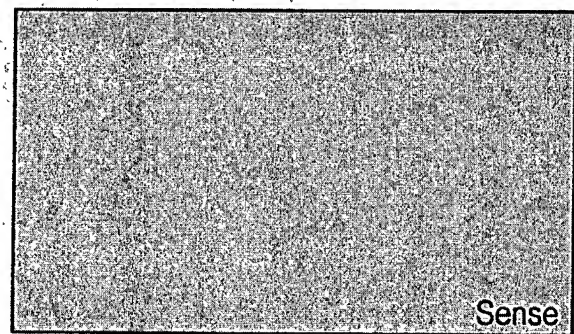


FIG. 14C-1

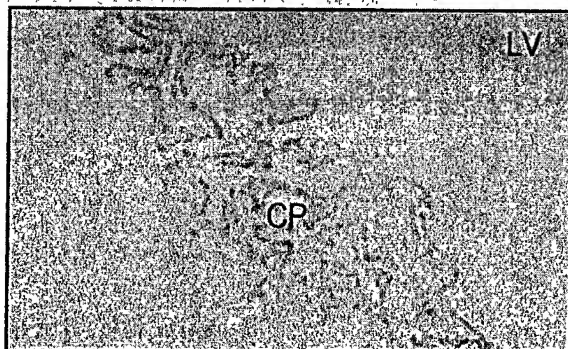
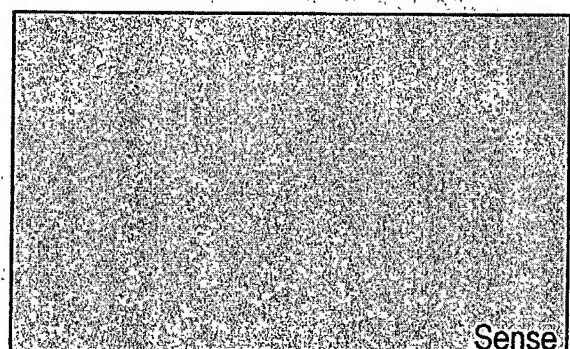


FIG. 14C-2



PATENT & TRADE-MARK

FIG. 14D-1

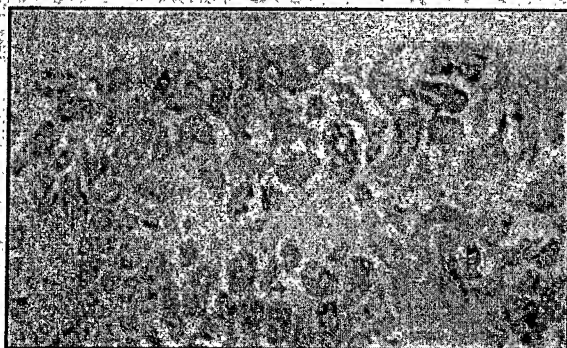


FIG. 14D-2



FIG. 14E

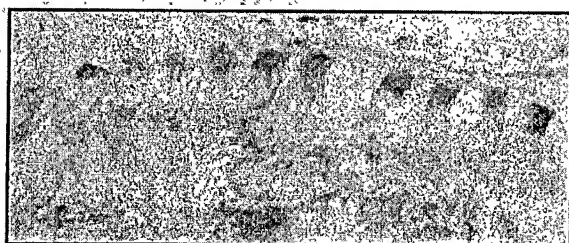


FIG. 14F

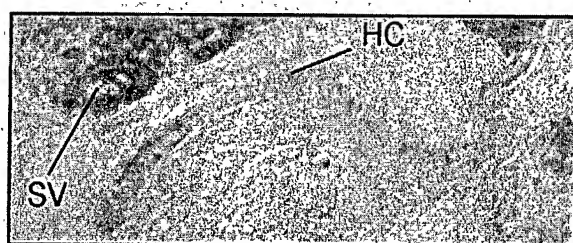




FIG. 15A
Osmotic avoidance/
basic paradigm

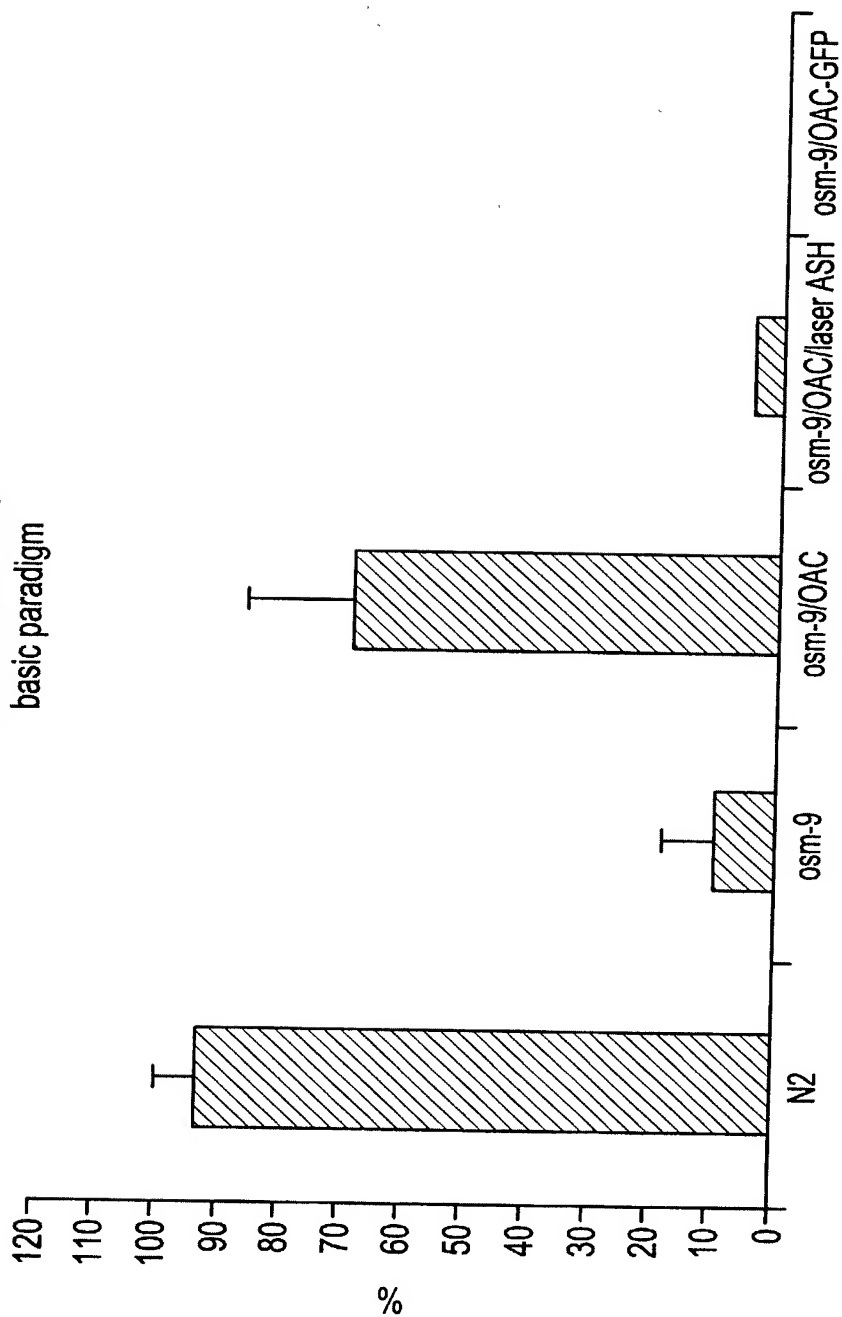


FIG. 15B

Nose touch
basic paradigm

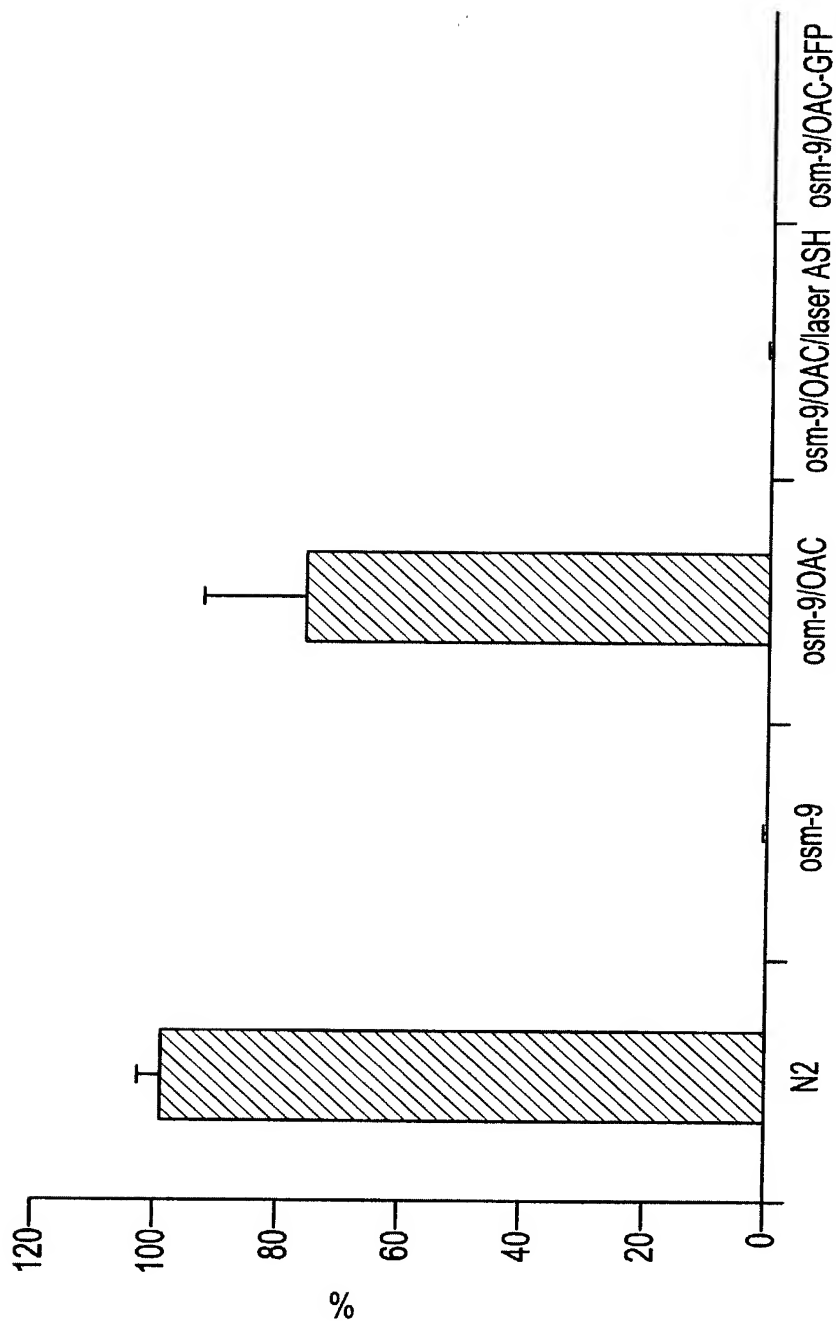




FIG. 16A

Nose touch
alternate mechanosensory pathway

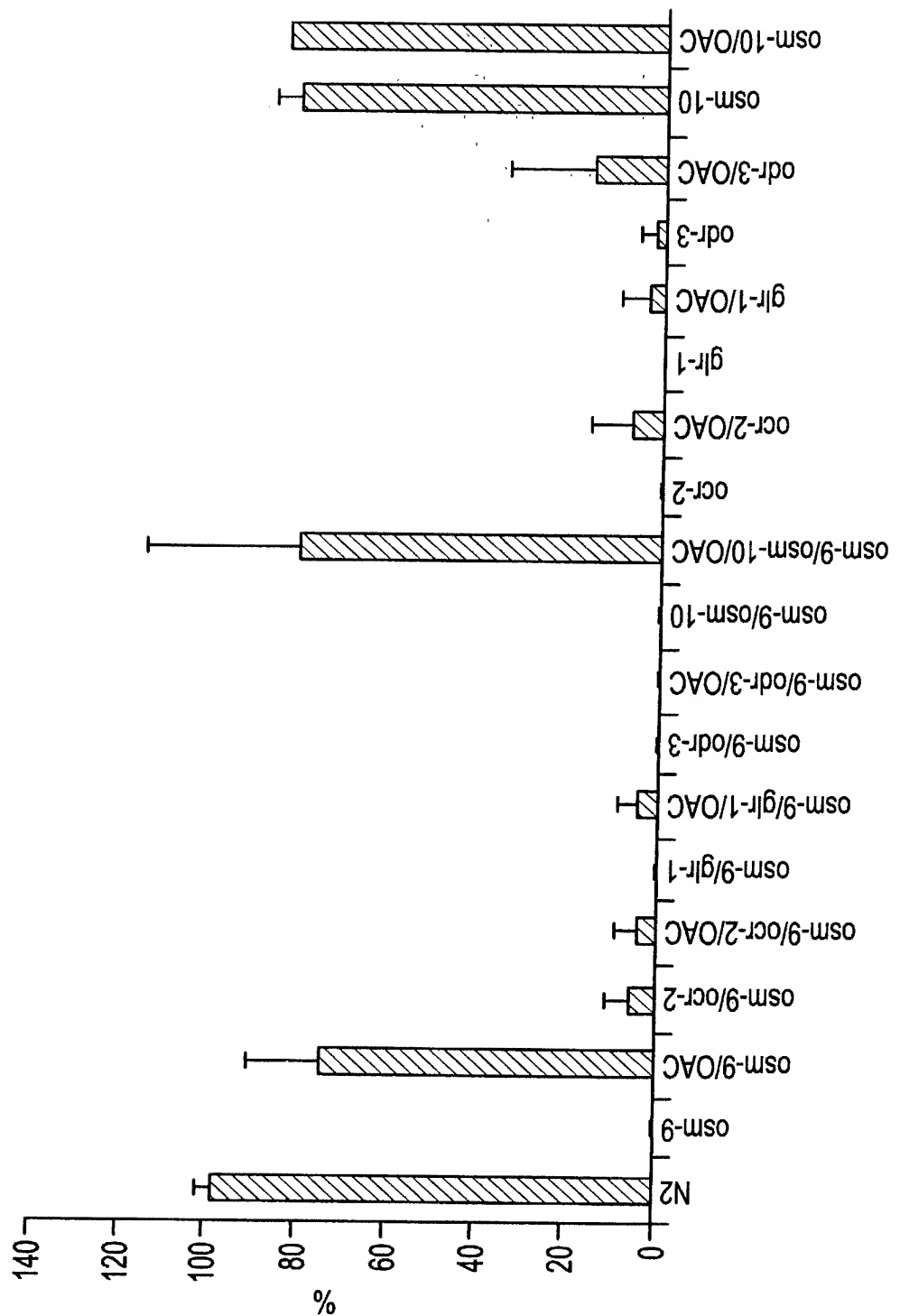




FIG. 16B

Osmotic avoidance
alternate mechanosensory pathway

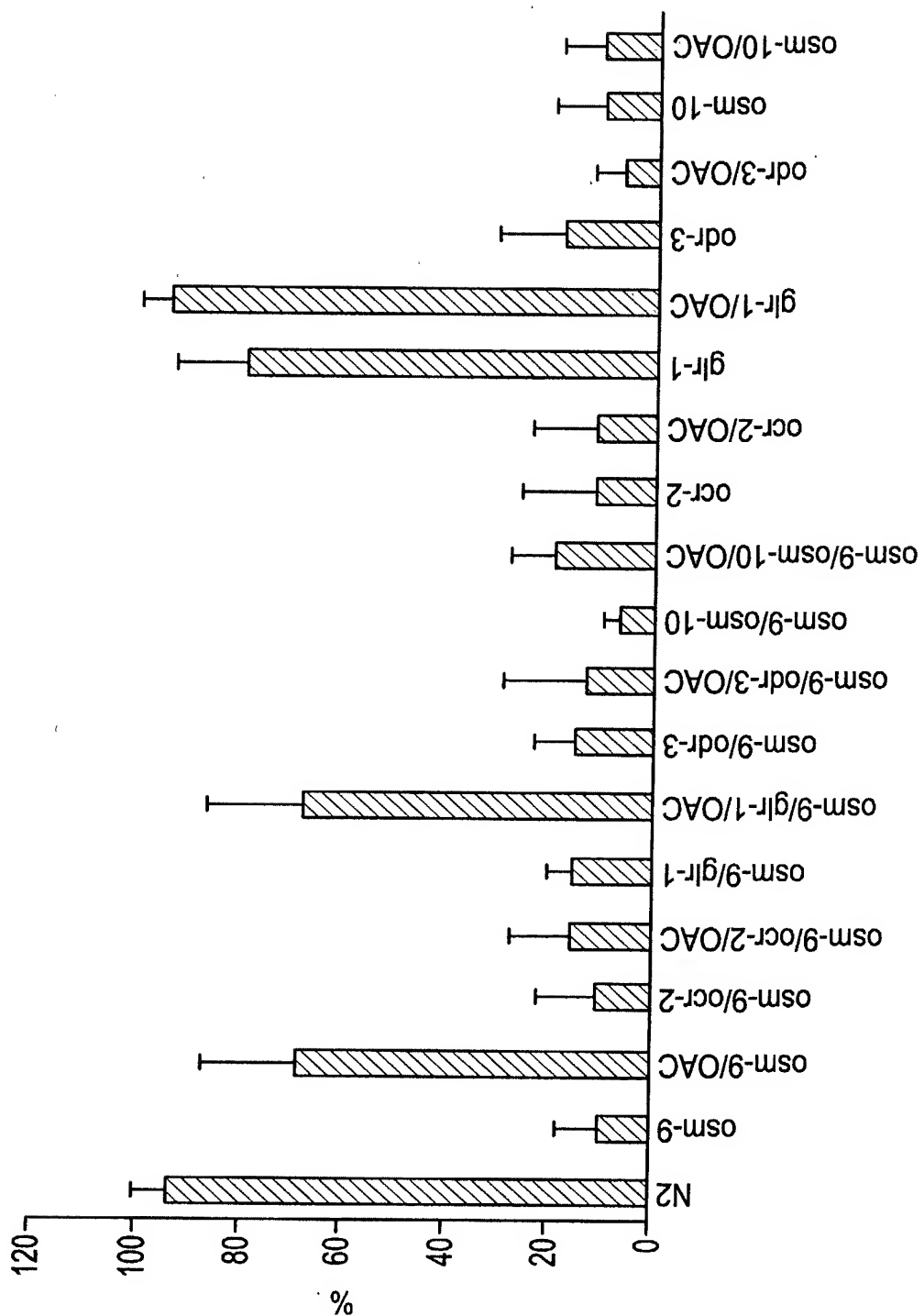




FIG. 17A
Osmotic avoidance
structure-function study

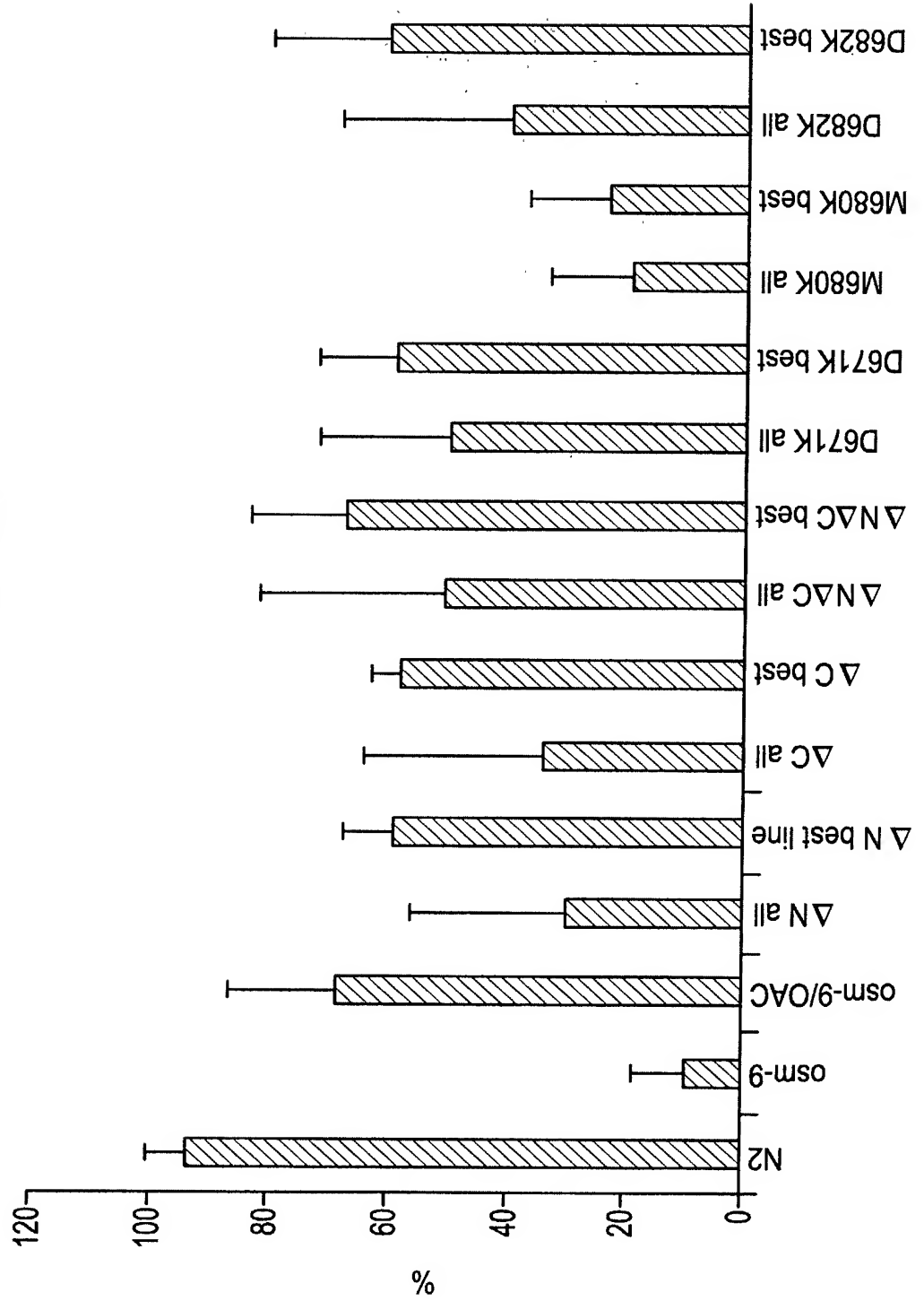




FIG. 17B
Nose touch
structure-function study

